

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Gruys, Kenneth J.

Mitsky, Timothy A.

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Slater, Steven C.

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(ii) TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate in Bacteria and Plants

(iii) NUMBER OF SEQUENCES: 11

25

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: St. Louis

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(D) STATE: Missouri

(E) COUNTRY: USA

(F) ZIP: 63167

(v) COMPUTER READABLE FORM:

35

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

5

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 13-MAR-1996

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(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Bond, Gary
- (B) REGISTRATION NUMBER: 29,283
- (C) REFERENCE/DOCKET NUMBER: 38-21(13585)A

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG

60

CTGCCGCAG CGGTTACGA GGCAGCGAG GTTACGCCGC TACAAAAAAT GGAAAAACTG

120

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	TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC	180
5	TTTAAGCTGC CGGGCGCATA CGCCATGATG GCAGGGCCTGA CGGAAGAACAA GAAAGCGCAC	240
	GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTC TTCTGCGCGG	300
	TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG	360
10	CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC	420
	AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG	480
	ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAACACTGC TCCAGCAGGA CGCCCATCTC	540
15	GACCGCGTAT TTGTGCCAGT CGGCGGGCGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC	600
	AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG	660
20	AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA	720
	GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC	780
	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGCGA TGAAGGATT ATTGAAAGAT	840
25	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC	900
	GCCCTGCACA ACATTGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC	960
30	TTCCACGGCC TGCCTACGT CTCAGAACGC TGCGAACCTGG TCGAACAGCG TGAAGCGTTG	1020
	TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC	1080
	GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAACGC CTGCATCTTT	1140
35	GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTGCA GATGCTAAC	1200
	GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC	1260

TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAATT	1320
CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT	1380
TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGGC GCGTACTGGC GGCGTTCGAA	1440
CTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC	1500
GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGGG GTTAA	1545

(2) INFORMATION FOR SEQ ID NO:2:

(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:2:

TTTTGGATC CGATATCTTA ACCCGCCAAA AAGAACCTGA ACGCCG 46

30 (2) INFORMATION FOR SEQ ID NO:3:

(A) DESCRIPTION: /desc = "synthetic DNA"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTGGATC CATGGCTGAC TCGCAACCCC TGTCCGG

37

10 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

25

CAGCTTCGAG TTCCCGGAAT CACCGGGCGC GTTCCTGCGC TTCC

44

(2) INFORMATION FOR SEQ ID NO:5:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5	ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATT AAGAGCAGTG	60
	CTGCGCGCGC CGGTTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG	120
	TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATGCCAGCC AGTGCACAGC	180
10	TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACAA GAAAGCGCAC	240
	GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTC TTCTGCGCGG	300
15	TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG	360
	CTGCGCGGCT TCGGCGCGA AGTGTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC	420
	AAAGCGATCG AACTGTACAA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG	480
20	ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAACTGC TCCAGCAGGA CGCCCATCTC	540
	GACCGCGTAT TTGTGCCAGT CGGCGCGCG GGTCTGGCTG CTTGCGTGGC GGTGCTGATC	600
25	AAACAACGTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAACG CGGAAGACTC CGCCTGCCTG	660
	AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA	720
	GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC	780
30	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGCGA TGAAGGATT ATTGAAAGAT	840
	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC	900
35	GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTG TTTCCGGTGC CAACGTGAAC	960
	TTCCACGGCC TGCCTACGT CTCAGAACGC TGCGAACTGG TCGAACAGCG TGAAGCGTTG	1020

	TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATCTGCCA ACTGCTTGGC	1080
	GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT	1140
5	GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTGCA GATGCTAAC	1200
	GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC	1260
	TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAGTTC	1320
10	CCGGAAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGTACGTA CTGGAACATT	1380
	TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGGC GCGTACTGGC GGCGTTCGAA	1440
15	CTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC	1500
	GACGAAACCA ATAACCCGGC GTTCAGGTTTC TTTTGCGGG GTTAA	1545
(2) INFORMATION FOR SEQ ID NO:6:		
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 65 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc = "synthetic DNA"	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
35	TATCGCAGCC ACGGCACCGA CTACGGGCGC GTACTGGCGG CGTTCGAATT TGGCGACCAT	60
	GAACC	65

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

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15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GGC GGCGCAG GTTACGCCGC TACAAAAAAAT GGAAAAAACTG 120

20

TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC 180

TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACAA GAAAGCGCAC 240

GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTC TTCTGCGCGG 300

25

TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGCGA AGTGCCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

30

AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAACTGC TCCAGCAGGA CGCCCATCTC 540

GACCGCGTAT TTGTGCCAGT CGGCGGGCGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600

35

AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720

	GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC	780
	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGCGA TGAAGGATT ATTGAAAGAT	840
5	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGAAATGAA AAAATATATC	900
	GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC	960
10	TTCCACGGCC TGCGCTACGT CTCAGAACGC TCGAACACTGG TCGAACAGCG TGAAGCGTTG	1020
	TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC	1080
	GGGCCTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT	1140
15	GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTAAC	1200
	GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC	1260
20	TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAATT	1320
	CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT	1380
	TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGGC GCGTACTGGC GGCCTTCGAA	1440
25	TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC	1500
	GACGAAACCA ATAACCCGGC GTTCAGGTTTC TTTTGCGGG GTTAA	1545

30 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG	60
	CTGCGCGCGC CGGTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAAT GGAAAAACTG	120
10	TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC	180
	TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACAA GAAAGCGCAC	240
15	GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTC TTCTGCGCGG	300
	TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG	360
	CTGCGGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC	420
20	AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG	480
	ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAACTGC TCCAGCAGGA CGCCCATCTC	540
25	GACCGCGTAT TTGTGCCAGT CGCGGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC	600
	AAACAACTGA TGCCCAAAT CAAAGTGATC GCCGTAGAAC CGGAAGACTC CGCCTGCCCTG	660
	AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA	720
30	GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC	780
	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGCGA TGAAGGATTT ATTGAAAGAT	840
35	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAAATGAA AAAATATATC	900
	GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC	960

	TTCCACGGCC TCGCCTACGT CTCAGAACGC TCGGAACCTGG TCGAACAGCG TGAAGCGTTG	1020
	TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC	1080
5	GGGC GTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT	1140
	GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTGCA GATGCTAAC	1200
	GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC	1260
10	TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAGTTC	1320
	CCGGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT	1380
15	TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGC GCGTACTGGC GGC GTTCGAA	1440
	TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC	1500
	GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGCGGG GTTAA	1545
20		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 1185 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGACCGCTG AAGTGGTAGT GGTAAGCGGT GTCCGTACCG CGATCGGGAC CTTTGGCGGC	60
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	AGCCTGAAGG ATGTGGCACCC GCGGAGCTG GGCGCACTGG TGGTGCACGA GCGCTGGCG	120
	CGCGCGCAGG TGTCGGCGA CGATGTCGGC CACGTGGTAT TCGGCAACGT GATCCAGACC	180
5	GAGCCGCGCG ACATGTATCT GGGCCGCGTC GCGGCCGTCA ACGGCGGGGT GACGATCAAC	240
	GCCCCCGCGC TGACCGTGAA CCGCCTGTGC GGCTCGGGCC TGCAGGCCAT TGTCAGCGCC	300
	GCGCAGACCA TCCTGCTGGG CGATACCGAC GTCGCCATCG GCGGCCGCGC GGAAAGCATG	360
10	AGCCGCCAC CGTACCTGGC GCGGCAGCG CGCTGGCGCG CACGCATGGG CGACGCCGGC	420
	CTGGTCGACA TGATGCTGGG TCGCCTGCAC GATCCCTTCC ATCGCATCCA CATGGCGTG	480
15	ACCGCCGAGA ATGTCGCCAA GGAATACGAC ATCTCGCGCG CGCAGCAGGA CGAGGCCGCG	540
	CTGGAATCGC ACCGCCGCGC TTCGGCAGCG ATCAAGGCCG GCTACTTCAA GGACCAGATC	600
	GTCCCCGTGG TGAGCAAGGG CCGCAAGGGC GACGTGACCT TCGACACCGA CGAGCACGTG	660
20	CGCCATGACG CCACCATCGA CGACATGACC AAGCTCAGGC CGGTCTTCGT CAAGGAAAAC	720
	GGCACGGTCA CGGCCGGCAA TGCCTCGGGC CTGAACGACG CGGCCGCCGC GGTGGTGATG	780
25	ATGGAGCGCG CGGAAGCCGA GCGCCGCGGC CTGAAGCCGC TGGCCCGCCT GGTGTCGTAC	840
	GGCCATGCCG GCGTGGACCC GAAGGCCATG GGCATCGGCC CGGTGCCGGC GACGAAGATC	900
	GCGCTGGAGC GCGCCGGCCT GCAGGTGTCG GACCTGGACG TGATCGAAGC CAACGAAGCC	960
30	TTTGCCGCAC AGGCGTGCAC CGTGACCAAG GCGCTCGGTC TGGACCCGGC CAAGGTTAAC	1020
	CCGAACGGCT CGGGCATCTC GCTGGGCCAC CCGATCGCG CGACCGGTGC CCTGATCAGC	1080
35	GTGAAGGCAC TGCATGAGCT GAACCGCGTG CAGGGCCGCT ACGCGCTGGT GACGATGTGC	1140
	ATCGCGGGCG GGCAGGGCAT TGCCGCCATC TTGAGCGTA TCTGA	1185

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- 5 (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Thr Arg Glu Val Val Val Ser Gly Val Arg Thr Ala Ile Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

35

Met Thr Arg Glu Val Val Val Ser Gly Val Arg Thr Ala Ile Gly
1 5 10 15

Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala
20 25 30

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Leu Val Val Arg Glu Ala Leu Ala Arg Ala Gln Val Ser Gly Asp Asp
35 40 45

5 Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp
50 55 60

Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn
65 70 75 80

10 Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala
85 90 95

Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala
15 100 105 110

Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro
115 120 125

20 Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met
130 135 140

Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val
145 150 155 160

25 Thr Ala Glu Asn Val Ala Lys Glu Tyr Asp Ile Ser Arg Ala Gln Gln
165 170 175

Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys
30 180 185 190

Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg
195 200 205

35 Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala
210 215 220

Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn

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Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala

245

250

255

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Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys

260

265

270

Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys

10

275

280

285

Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg

290

295

300

15

Ala Gly Leu Gln Val Ser Asp Leu Asp Val Ile Glu Ala Asn Glu Ala

305

310

315

320

Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro

325

330

335

20

Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile

340

345

350

Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn

25

355

360

365

Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly

370

375

380

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Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile

385

390

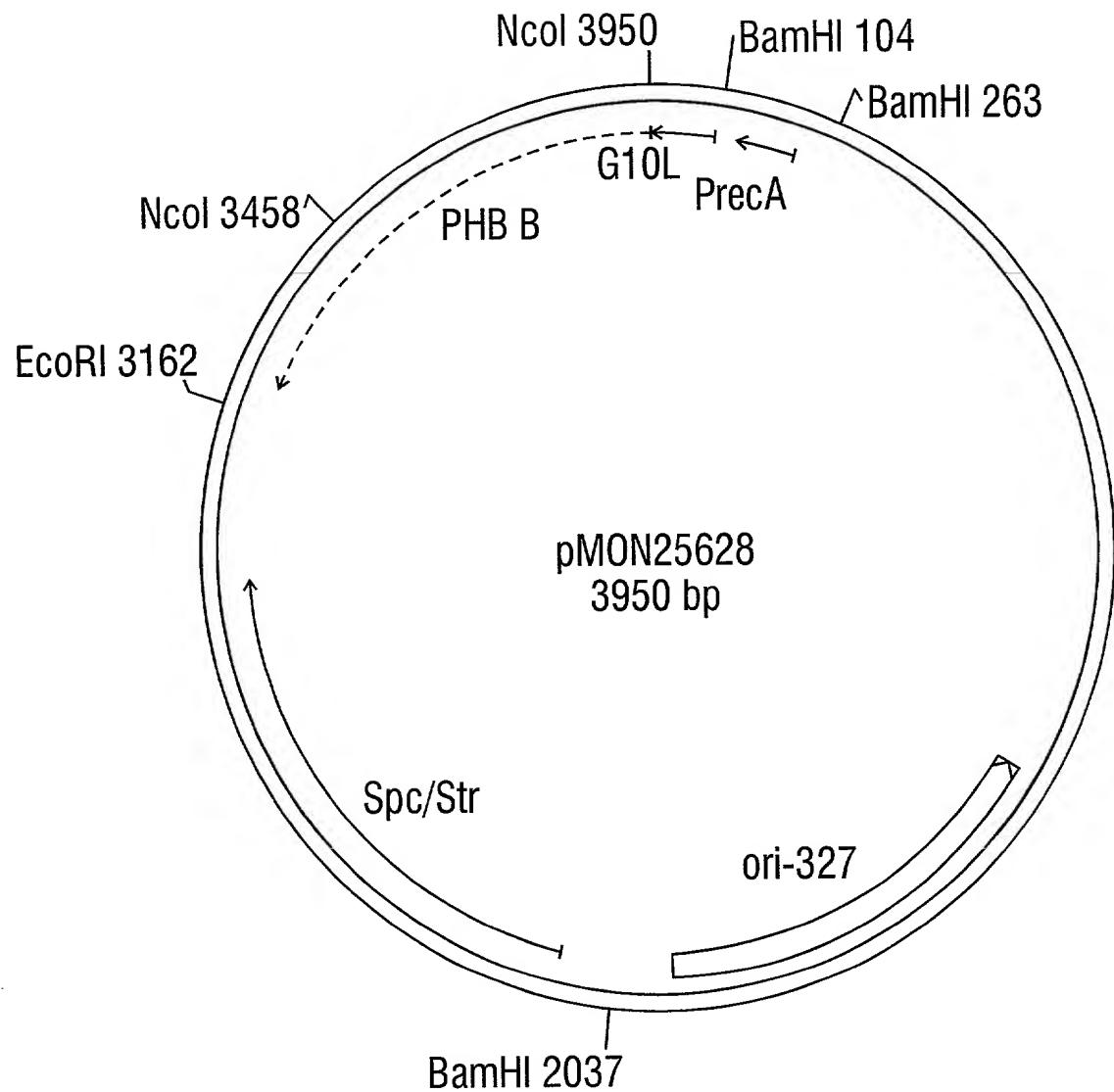


FIG. 18

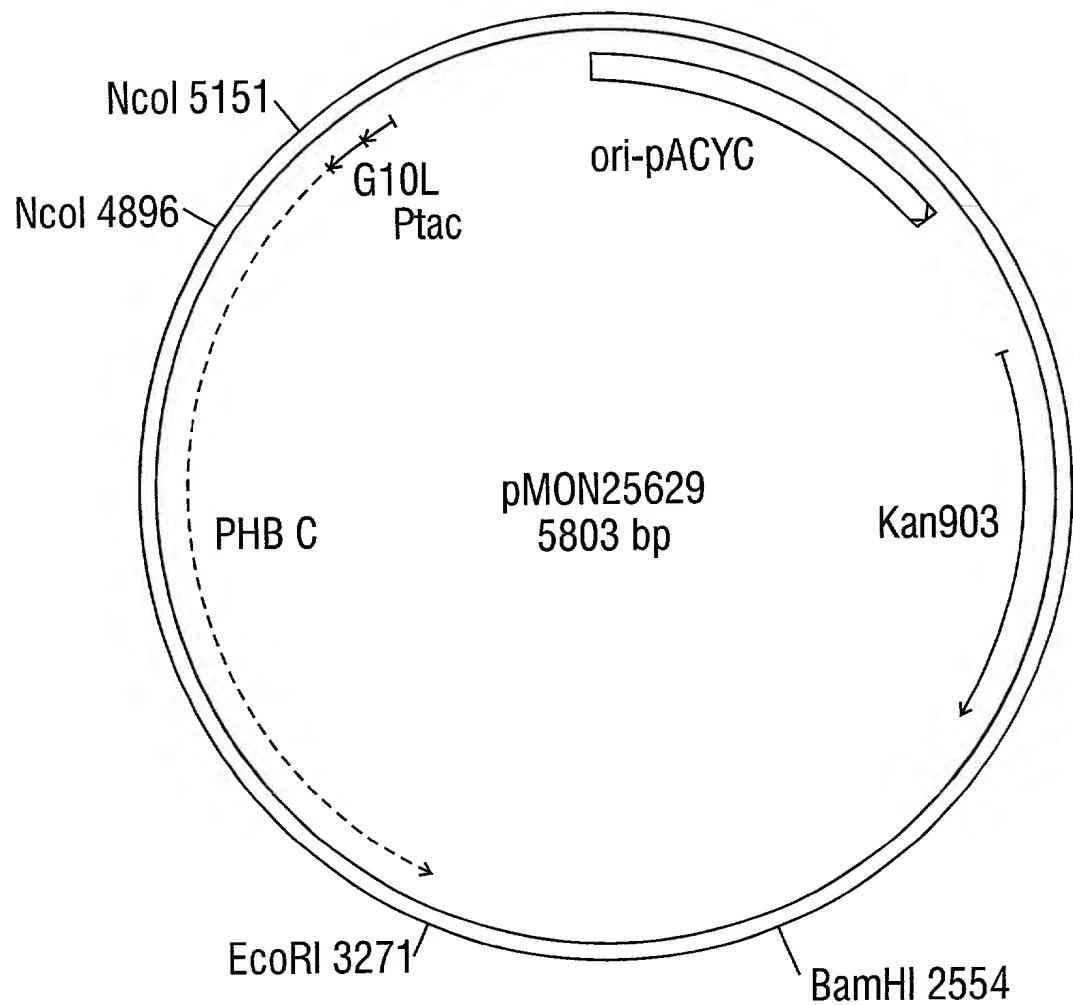


FIG. 19

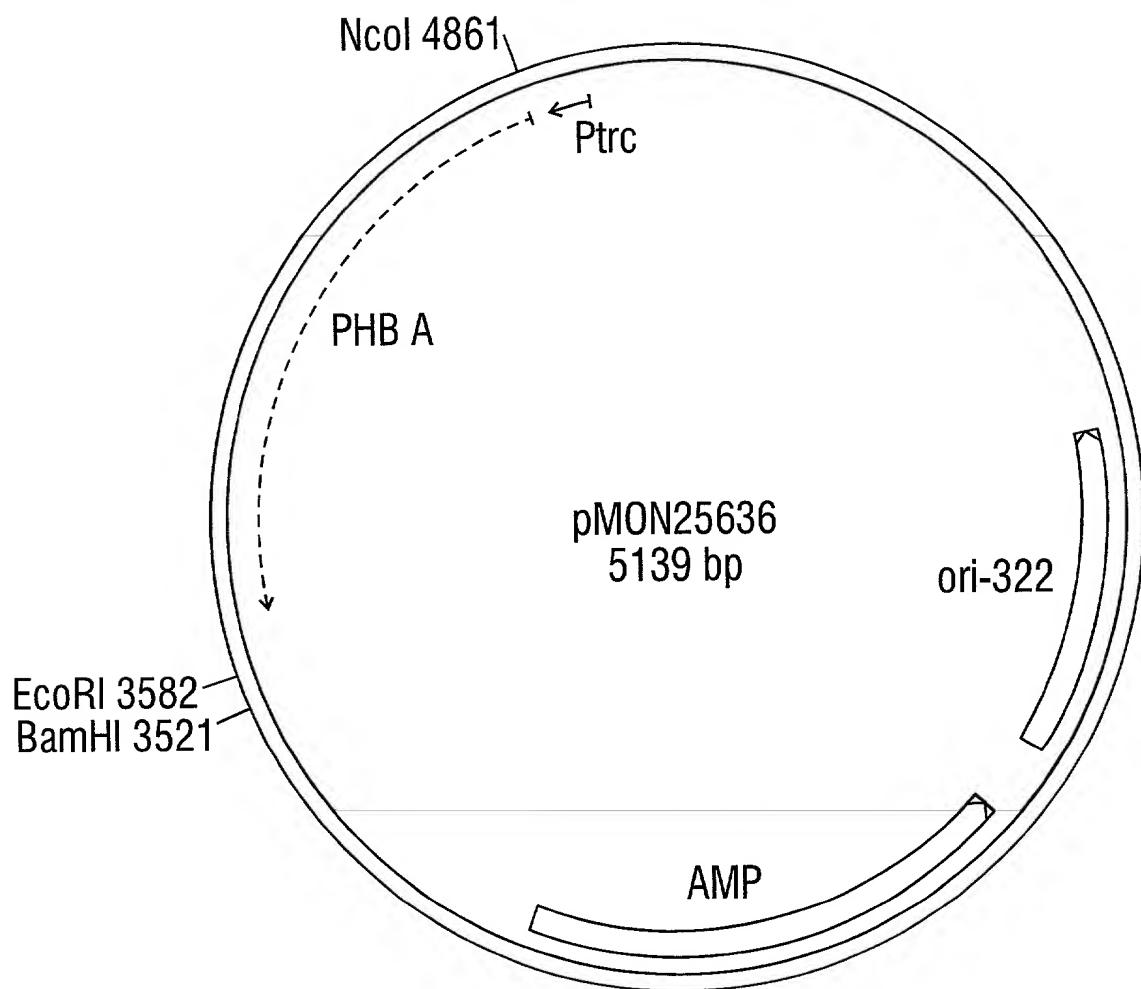


FIG. 20

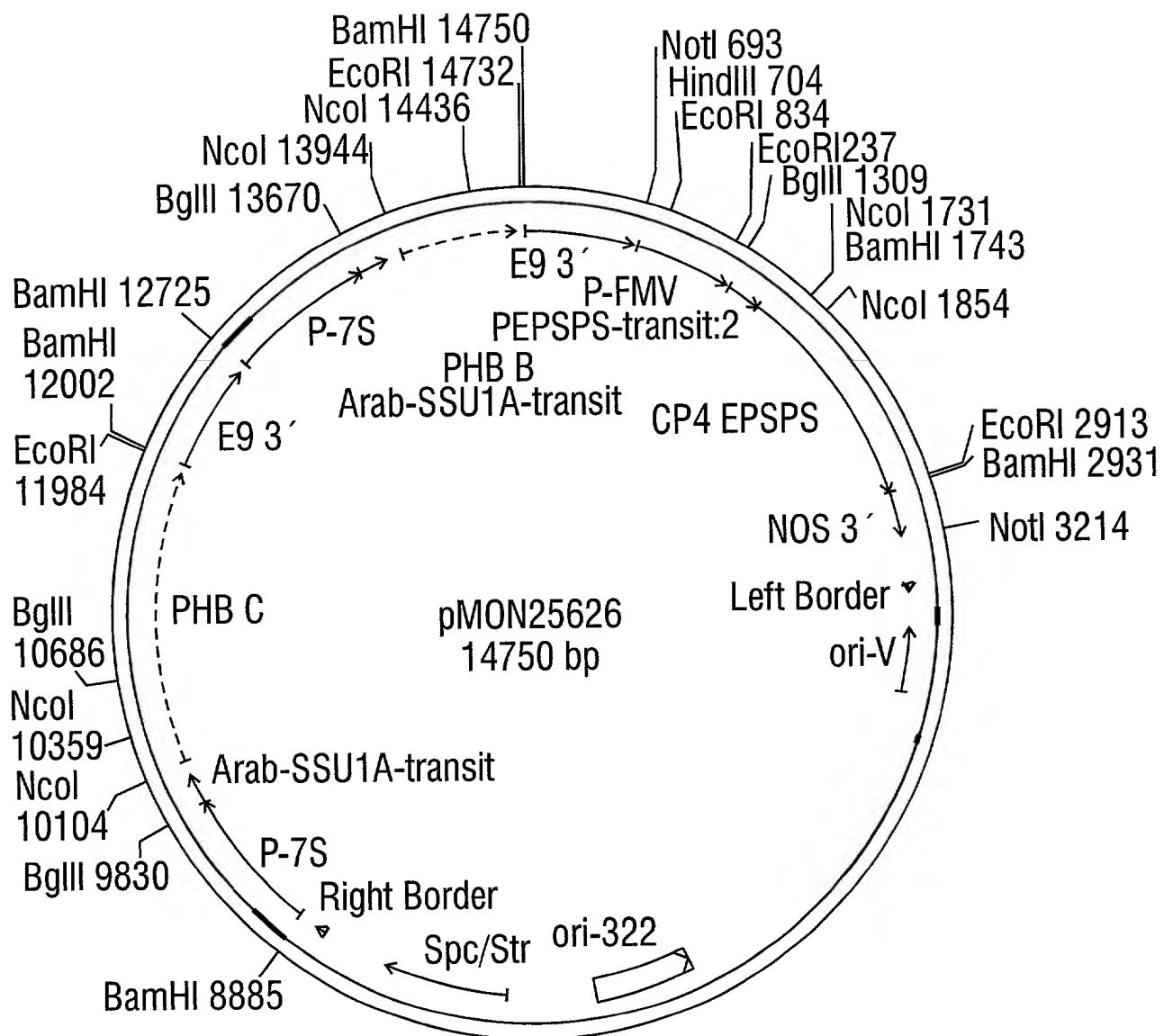


FIG. 21

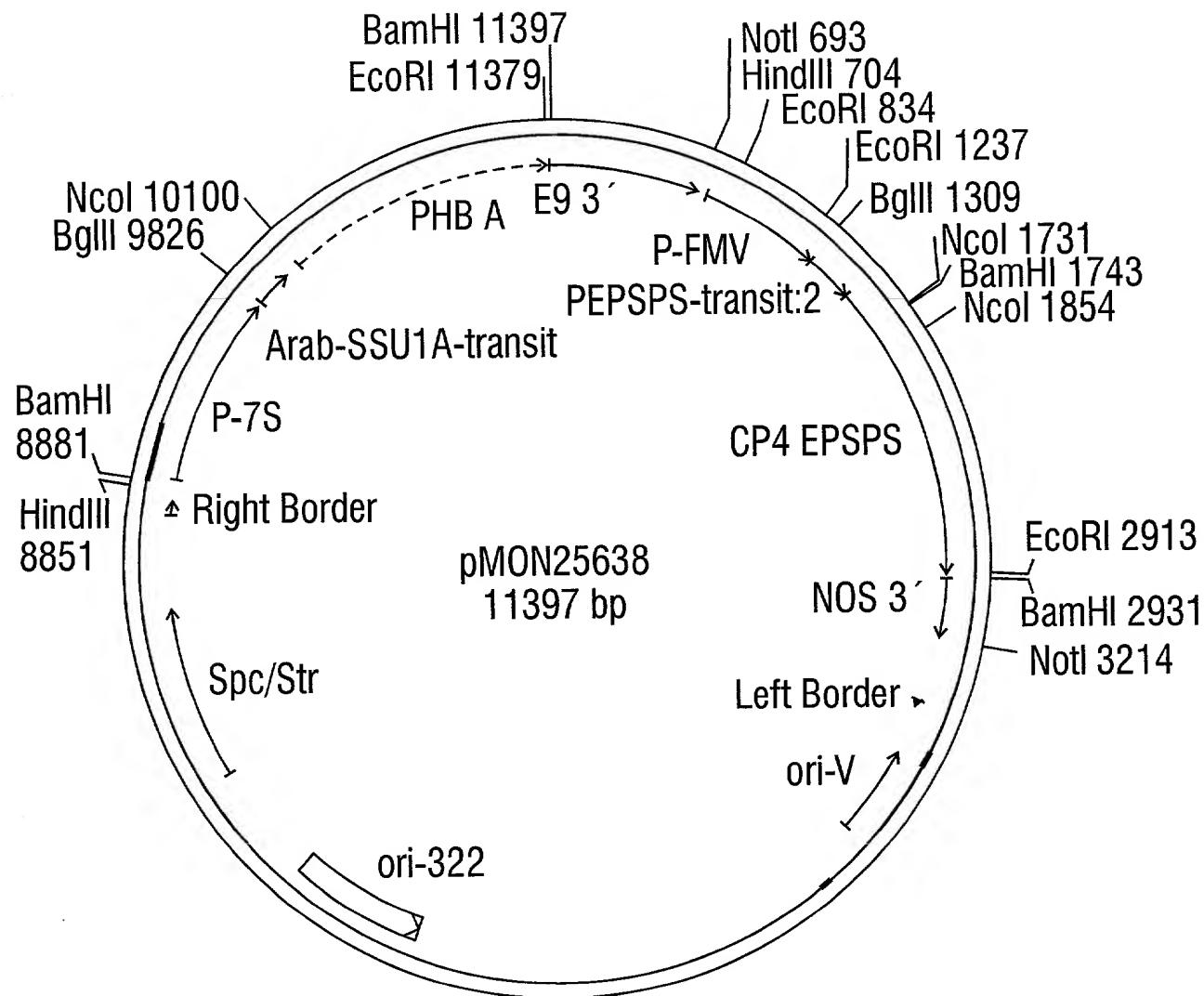


FIG. 22